



9

SEQUENCE LISTING

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TECH CENTER 1600/2900

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<120> Novel GPCR-Like Proteins and Nucleic Acids Encoding
Same

<130> 21402-224 AG

<140> 10/024444

<141> 2001-12-18

<150> 60/256635

<151> 2000-12-18

<160> 12

<170> PatentIn Ver. 2.1

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<212> DNA

<213> Unknown Organism

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<223> Description of Unknown Organism: Unknown

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gtccacatg cccatgtacc tcctgcttgg gcagctctct ctcatggacc tcctgttcac 240
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cctcatgagc ccaagagtct gctggatcat ggtggccaca tcctggatcc tggcatccct 480
gattgctata ggacatacca tgtacactat gcacctccct ttctgtgtgt cctgggaaat 540
caggcatctg ctctgtgaga tcccaccctt gctgaagttg gcctgtgctg atacctccag 600
gtatgagctt ataataacg tgacaggtgt gactttcctc ttgctcccca tttctgccat 660
tgtggcctcc tacacactag tcctattcac tgtgcttcgt atgccatcaa atgaggggag 720
gaagaaagcc cttgtcacct gctcttccca cctgattgtg gtcgggatgt tctatggagc 780
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<220>
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 35 40 45
 Ile Thr Ile Glu Ala Arg Leu His Met Pro Met Tyr Leu Leu Leu Gly
 50 55 60
 Gln Leu Ser Leu Met Asp Leu Leu Phe Thr Ser Val Val Thr Pro Lys
 65 70 75 80
 Ala Leu Ala Asp Phe Leu Arg Arg Glu Asn Thr Ile Ser Phe Gly Gly
 85 90 95
 Cys Ala Leu Gln Met Phe Leu Ala Leu Thr Met Gly Ser Ala Glu Asp
 100 105 110
 Leu Leu Leu Ala Phe Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
 115 120 125
 Pro Leu Lys Tyr Met Thr Leu Met Ser Pro Arg Val Cys Trp Ile Met
 130 135 140
 Val Ala Thr Ser Trp Ile Leu Ala Ser Leu Ile Ala Ile Gly His Thr
 145 150 155 160
 Met Tyr Thr Met His Leu Pro Phe Cys Val Ser Trp Glu Ile Arg His
 165 170 175
 Leu Leu Cys Glu Ile Pro Pro Leu Leu Lys Leu Ala Cys Ala Asp Thr
 180 185 190
 Ser Arg Tyr Glu Leu Ile Ile Tyr Val Thr Gly Val Thr Phe Leu Leu
 195 200 205
 Leu Pro Ile Ser Ala Ile Val Ala Ser Tyr Thr Leu Val Leu Phe Thr
 210 215 220
 Val Leu Arg Met Pro Ser Asn Glu Gly Arg Lys Lys Ala Leu Val Thr
 225 230 235 240
 Cys Ser Ser His Leu Ile Val Val Gly Met Phe Tyr Gly Ala Ala Thr

Ser Arg Tyr Glu Leu Met Val Tyr Val Met Gly Val Thr Phe Leu Ile
 195 200 205
 Pro Ser Leu Ala Ala Ile Leu Ala Ser Tyr Thr Gln Ile Leu Leu Thr
 210 215 220
 Val Leu His Met Pro Ser Asn Glu Gly Arg Lys Lys Ala Leu Val Thr
 225 230 235 240
 Cys Ser Ser His Leu Thr Val Val Gly Met Phe Tyr Gly Ala Ala Thr
 245 250 255
 Phe Met Tyr Val Leu Pro Ser Ser Phe His Ser Thr Arg Gln Asp Asn
 260 265 270
 Ile Ile Ser Val Phe Tyr Thr Ile Val Thr Pro Ala Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Glu Val Met Arg Ala Leu Arg Arg Val
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 Ala Leu Tyr Met Leu Ala Leu Ile Ser Asn Gly Leu Leu Leu Val
 35 40 45
 Ile Thr Val Asp Ala Arg Leu His Val Pro Met Tyr Leu Leu Leu Arg
 50 55 60
 Gln Leu Ser Leu Ile Asp Leu Leu Phe Thr Ser Val Val Thr Pro Lys
 65 70 75 80
 Ala Val Met Asp Phe Leu Leu Arg Asp Asn Thr Ile Ser Phe Gly Gly
 85 90 95
 Cys Ala Leu Gln Met Ala Leu Ala Leu Met Leu Gly Ser Ala Glu Asp
 100 105 110
 Leu Leu Leu Ala Phe Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
 115 120 125
 Pro Leu Asn Tyr Met Val Phe Met Ser Pro Thr Val Cys Trp Leu Ile
 130 135 140

Val Ser Thr Ser Trp Ile Leu Ala Ser Leu Thr Ala Val Gly His Thr
 145 150 155 160
 Val Tyr Thr Met His Phe Pro Phe Cys Met Ser Gln Glu Ile Arg His
 165 170 175
 Leu Leu Cys Glu Ile Leu Pro Leu Leu Lys Leu Ser Cys Val Asp Thr
 180 185 190
 Ser Gln Tyr Glu Leu Met Val Tyr Val Thr Gly Val Thr Phe Leu Leu
 195 200 205
 Leu Pro Leu Ser Ala Ile Val Thr Ser Tyr Thr Leu Ile Leu Ser Thr
 210 215 220
 Val Leu His Met Pro Ser Asn Glu Gly Lys Lys Lys Ala Leu Val Thr
 225 230 235 240
 Cys Leu Ser His Leu Met Val Val Gly Met Phe Tyr Gly Ala Ala Thr
 245 250 255
 Phe Met Tyr Val Leu Pro Ser Ser Leu His Ser Ala Lys Gln Asp Asn
 260 265 270
 Ile Ile Ser Val Phe Tyr Thr Ile Val Thr Pro Ala Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Glu Val Ile Gly Ala Leu Arg Arg Val
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 Leu Gly Arg Tyr Ile Leu Pro Ala His Leu Thr Leu
 305 310 315

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 Thr Leu Tyr Met Leu Ala Leu Ile Ser Asn Gly Leu Leu Leu Leu Val
 35 40 45
 Ile Thr Val Asp Ala Arg Leu His Val Pro Met Tyr Leu Leu Leu Arg
 50 55 60
 Gln Leu Ser Leu Ile Asp Leu Leu Phe Thr Ser Val Val Thr Pro Asn
 65 70 75 80
 Thr Val Val Asp Phe Leu Leu Arg Asp Asn Thr Ile Ser Phe Glu Gly

| 85 | | | | | | | | | | 90 | | | | | 95 | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|
| Cys | Ala | Leu | Gln | Leu | Phe | Ser | Ala | Met | Thr | Leu | Gly | Gly | Ala | Glu | Asp | | | | |
| | | | 100 | | | | | 105 | | | | | | 110 | | | | | |
| Leu | Leu | Leu | Ala | Phe | Met | Ala | Tyr | Asp | Arg | Tyr | Val | Ala | Ile | Cys | His | | | | |
| | | 115 | | | | | 120 | | | | | | 125 | | | | | | |
| Pro | Leu | Asn | Tyr | Met | Ile | Phe | Met | Ser | Pro | Lys | Ala | Cys | Arg | Leu | Met | | | | |
| | 130 | | | | | 135 | | | | | 140 | | | | | | | | |
| Val | Ala | Ile | Ser | Trp | Ile | Leu | Ala | Ser | Leu | Ser | Ala | Leu | Gly | His | Thr | | | | |
| 145 | | | | | 150 | | | | | | 155 | | | | 160 | | | | |
| Val | Tyr | Thr | Met | His | Phe | Pro | Phe | Cys | Met | Ser | Gln | Glu | Ile | Arg | His | | | | |
| | | | | 165 | | | | | 170 | | | | | 175 | | | | | |
| Leu | Leu | Cys | Glu | Val | Pro | Pro | Leu | Leu | Lys | Leu | Ala | Cys | Ala | Asp | Thr | | | | |
| | | | 180 | | | | | 185 | | | | | | 190 | | | | | |
| Ser | Gln | Tyr | Glu | Leu | Met | Val | Tyr | Val | Thr | Gly | Val | Ile | Phe | Leu | Leu | | | | |
| | | 195 | | | | | 200 | | | | | 205 | | | | | | | |
| Leu | Pro | Leu | Ser | Ala | Ile | Ile | Thr | Ser | Tyr | Ser | Leu | Ile | Leu | Phe | Thr | | | | |
| | 210 | | | | | 215 | | | | | 220 | | | | | | | | |
| Val | Leu | His | Met | Pro | Ser | Asn | Glu | Gly | Arg | Lys | Lys | Ala | Leu | Val | Thr | | | | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | | | | |
| Cys | Ser | Ser | His | Leu | Thr | Val | Val | Gly | Met | Phe | Tyr | Gly | Gly | Ala | Thr | | | | |
| | | | | 245 | | | | | 250 | | | | | 255 | | | | | |
| Phe | Met | Tyr | Val | Leu | Pro | Ser | Ser | Phe | His | Ser | Pro | Lys | Gln | Asp | Asn | | | | |
| | | | 260 | | | | | 265 | | | | | | 270 | | | | | |
| Ile | Ile | Ser | Val | Phe | Tyr | Thr | Ile | Val | Thr | Pro | Ala | Leu | Asn | Pro | Leu | | | | |
| | | 275 | | | | | 280 | | | | | | 285 | | | | | | |
| Ile | Tyr | Ser | Leu | Arg | Asn | Lys | Glu | Val | Ile | Gly | Ala | Val | Arg | Arg | Val | | | | |
| | 290 | | | | | 295 | | | | | 300 | | | | | | | | |
| Leu | Gly | Arg | His | Ile | Leu | Pro | Ala | His | Ala | Thr | Val | | | | | | | | |
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 35 40 45
 Ile Thr Val Asp Ala Arg Leu His Val Pro Met Tyr Leu Leu Leu Arg
 50 55 60
 Gln Leu Ser Leu Ile Asp Leu Leu Phe Thr Ser Val Val Thr Pro Asn
 65 70 75 80
 Thr Val Val Asp Phe Leu Leu Arg Asp Asn Thr Ile Ser Phe Glu Gly
 85 90 95
 Cys Ala Leu Gln Leu Phe Ser Ala Met Thr Leu Gly Gly Ala Glu Glu
 100 105 110
 Leu Leu Leu Ala Phe Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
 115 120 125
 Pro Leu Asn Tyr Met Ile Phe Met Ser Pro Lys Ala Cys Arg Leu Met
 130 135 140
 Val Ala Ile Ser Trp Ile Leu Ala Ser Leu Ser Ala Leu Gly His Thr
 145 150 155 160
 Val Tyr Thr Met His Phe Pro Phe Cys Met Ser Gln Glu Ile Arg His
 165 170 175
 Leu Leu Cys Glu Val Pro Pro Leu Leu Lys Leu Ala Cys Ala Asp Thr
 180 185 190
 Ser Gln Tyr Glu Leu Met Val Tyr Val Thr Gly Val Ile Phe Leu Leu
 195 200 205
 Leu Pro Leu Ser Ala Ile Ile Thr Ser Tyr Ser Leu Ile Leu Phe Thr
 210 215 220
 Val Leu His Met Pro Ser Asn Glu Gly Arg Lys Lys Ala Leu Val Thr
 225 230 235 240
 Cys Ser Ser His Leu Thr Val Val Gly Met Phe Tyr Gly Gly Ala Thr
 245 250 255
 Phe Met Tyr Val Leu Pro Ser Ser Phe His Ser Pro Lys Gln Asp Asn
 260 265 270
 Ile Ile Ser Val Phe Tyr Thr Ile Val Thr Pro Ala Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Glu Val Ile Gly Ala Val Arg Arg Val
 290 295 300
 Leu Gly Arg His Ile Leu Pro Ala His Ala Thr Val
 305 310 315

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Ile Ile Ser Val Phe Tyr Thr Ile Val Thr Pro Ala Leu Asn Pro Leu
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Ile Tyr Ser Leu Arg Asn Lys Glu Val Thr Gly Ala Leu Ile Arg Val
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Leu Gly Arg Tyr Ile Val Pro Ala His Pro Thr Leu
305 310 315

<210> 8

<211> 17

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Protein motif

<220>

<221> VARIANT

<222> (1)

<223> X1 wherein X aa is G, or S, or T, or A, or L, or
I, or V, or M, or F, or Y, or W, or C

<220>

<221> VARIANT

<222> (2)

<223> X2 wherein X aa is G, or S, or T, or A, or N, or
C, or P, or D, or E

<220>

<221> VARIANT

<222> (3)

<223> X3 wherein X aa is E, or D, or P, or K, or R, or H

<220>

<221> VARIANT

<222> (4)

<223> X4 wherein X aa is any amino acid

<220>

<221> VARIANT

<222> (5)

<223> X5 wherein X aa is any amino acid

<220>

<221> VARIANT

<222> (6)

<223> X6 wherein X aa is L, or I, or V, or M, or N, or
Q, or G, or A

<220>

<221> VARIANT

<222> (7)

<223> X7 wherein X aa is any amino acid

<220>

<221> VARIANT

<222> (8)

<223> X8 wherein X is any amino acid

<220>

<221> VARIANT

<222> (9)

<223> X9 wherein X aa is L, or I, or V, or M, or F, or T

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<221> VARIANT

<222> (10)

<223> X10 wherein Xaa is G, or S, or T, or A, or N, or C

<220>

<221> VARIANT

<222> (11)

<223> X11 wherein Xaa is L, or I, or V, or M, or F, or
Y, or W, or S, or T, or A, or C

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<221> VARIANT

<222> (12)

<223> X12 wherein X aa is D, or E, or N, or H

<220>

<221> VARIANT

<222> (14)

<223> X13 wherein X aa is F, or Y, or W, or C, or S, or
H

<220>

<221> VARIANT

<222> (15)

<223> X14 wherein X aa is any amino acid

<220>

<221> VARIANT

<222> (16)

<223> X15 wherein X aa is any amino acid

<220>

<221> VARIANT

<222> (17)

<223> X16 wherein X aa is L, or I or V, or M

<400> 8

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1

5

10

15

Xaa

<210> 9

<211> 254

<212> PRT

<213> Unknown Organism

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      20              25              30

Phe Leu Leu Thr Leu Pro Pro Trp Ala Leu Tyr Tyr Leu Val Gly Gly
      35              40              45

Asp Trp Val Phe Gly Asp Ala Leu Cys Lys Leu Val Gly Ala Leu Phe
      50              55              60

Val Val Asn Gly Tyr Ala Ser Ile Leu Leu Leu Thr Ala Ile Ser Ile
      65              70              75              80

Asp Arg Tyr Leu Ala Ile Val His Pro Leu Arg Tyr Arg Arg Ile Arg
      85              90              95

Thr Pro Arg Arg Ala Lys Val Leu Ile Leu Leu Val Trp Val Leu Ala
      100             105             110

Leu Leu Leu Ser Leu Pro Pro Leu Leu Phe Ser Trp Leu Arg Thr Val
      115             120             125

Glu Glu Gly Asn Thr Thr Val Cys Leu Ile Asp Phe Pro Glu Glu Ser
      130             135             140

Val Lys Arg Ser Tyr Val Leu Leu Ser Thr Leu Val Gly Phe Val Leu
      145             150             155             160

Pro Leu Leu Val Ile Leu Val Cys Tyr Thr Arg Ile Leu Arg Thr Leu
      165             170             175

Arg Lys Arg Ala Arg Ser Gln Arg Ser Leu Lys Arg Arg Ser Ser Ser
      180             185             190

Glu Arg Lys Ala Ala Lys Met Leu Leu Val Val Val Val Val Phe Val
      195             200             205

Leu Cys Trp Leu Pro Tyr His Ile Val Leu Leu Leu Asp Ser Leu Cys
      210             215             220

Leu Leu Ser Ile Trp Arg Val Leu Pro Thr Ala Leu Leu Ile Thr Leu
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Trp Leu Ala Tyr Val Asn Ser Cys Leu Asn Pro Ile Ile Tyr
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<211> 22

<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: PCR Primer

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22

<210> 11

<211> 26

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: PCR Primer

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26

<210> 12

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

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ggctggagtg acaattgtgt ag

22